

EXHIBIT "F"

FASTA searches a protein or DNA sequence data bank
 version 3.3t05 March 30, 2000
 Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAACZaWfX: 1219 aa
 >SEQ ID NO 23 human transporter
 vs /tmp/fastaDAADZaWfX library
 searching /tmp/fastaDAADZaWfX library

1382 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 40, opt: 28, gap-pen: -12/ -2, width: 16
 Scan time: 0.050

The best scores are: opt
 gi|21729873|ref|NP_115972.2| ATP-binding cassette (1382) 4838

>>gi|21729873|ref|NP_115972.2| ATP-binding cassette, sub (1382 aa)
 initn: 7928 initl: 4838 opt: 4838
 Smith-Waterman score: 7606; 88.061% identity in 1382 aa overlap (1-1219:1-1382)

	10	20	30	40	50	60
SEQ	MTRKRTYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP					
					
gi 217	MTRKRTYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP					
	10	20	30	40	50	60
	70	80	90	100	110	120
SEQ	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL					
					
gi 217	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
SEQ	SVHDASDKNVQRLHRLWEEVSRRGIEKASVLLVMLRFQRTLRIFDALLGICFCIASVLG					
					
gi 217	SVHDASDKNVQRLHRLWEEVSRRGIEKASVLLVMLRFQRTLRIFDALLGICFCIASVLG					
	130	140	150	160	170	180
	190	200	210	220	230	240
SEQ	PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFQAAVSS					
					
gi 217	PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAVSS					
	190	200	210	220	230	240
	250	260	270	280	290	300
SEQ	FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSEYFIIG					
					
gi 217	FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSEYFIIG					
	250	260	270	280	290	300
	310	320	330	340	350	360
SEQ	YTAFIAILCYLLVFPLEVFMTMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKP					
					
gi 217	YTAFIAILCYLLVFPPLAVFMTRMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKP					
	310	320	330	340	350	360
	370	380	390	400	410	420
SEQ	FAKIIEDLRRKERKLLKCGLVQSLTSITLFIIPTVATAVVWLIHTSLKLTASMAFSM					
					
gi 217	FAKIIEDLRRKERKLLKCGLVQSLTSITLFIIPTVATAVVWLIHTSLKLTASMAFSM					
	370	380	390	400	410	420

	430	440	450	460	470	480
SEQ	LASLNLLRLSVFFVPIAVKGLTNSKSAVMRFFKKFFLQESPVFYVQTLQDPSKALVFEEAT					
gi 217	LASLNLLRLSVFFVPIAVKGLTNSKSAVMRFFKKFFLQESPVFYVQTLQDPSKALVFEEAT					
	430	440	450	460	470	480

	490	500	510	520	530	540
SEQ	LSWQQTCPGIVNGALELERNGHASEGMTRPRDALGPEEEGNSLGPELHKINLVVSKGMML					
gi 217	LSWQQTCPGIVNGALELERNGHASEGMTRPRDALGPEEEGNSLGPELHKINLVVSKGMML					
	490	500	510	520	530	540

	550	560	570	580	590	600
SEQ	GVCNGTSGSKSSLLSAILEEMHLLGSGVGVQGLAYVPPQAWIVSGNIRENILMGGAYDK					
gi 217	GVCNGTSGSKSSLLSAILEEMHLLGSGVGVQGLAYVPPQAWIVSGNIRENILMGGAYDK					
	550	560	570	580	590	600

	610	620	630	640	650	660
SEQ	ARYLQVLHCCSLNRDLELLPFGDMTEIGERGLNLSGGQKQRISLARAVYSDRQIYLLDDP					
gi 217	ARYLQVLHCCSLNRDLELLPFGDMTEIGERGLNLSGGQKQRISLARAVYSDRQIYLLDDP					
	610	620	630	640	650	660

	670	680	690	700	710	720
SEQ	LSAVDAHVGKHIFECEIKKTLRGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELM					
gi 217	LSAVDAHVGKHIFECEIKKTLRGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELM					
	670	680	690	700	710	720

	730					
SEQ	QKKGKYAQLIQMHKEATS-----					
gi 217	QKKGKYAQLIQMHKEATS-----					
	730	740	750	760	770	780

SEQ	-----					
gi 217	EEMEEGSLSWRVYHHYIQAAGGYMVSCIIFFFVVLIVFLTIFSFWWLSYWLEQSGGTNSS					
	790	800	810	820	830	840

SEQ	-----					
gi 217	RESNGTMADLGNIADNPQLSFYQLVYGLNALLLICVGVCSGIFTKVTRKASTALHNKLF					
	850	860	870	880	890	900

	740	750	760	770	780	790
SEQ	--VFRCPMSFFDTIPIGRLLNCFAGDLEQLDQLLPFIQFLVLSLMVIAVLLIVSVLSP					
gi 217	NKVFRCPMSFFDTIPIGRLLNCFAGDLEQLDQLLPFIQFLVLSLMVIAVLLIVSVLSP					
	910	920	930	940	950	960

	800	810	820	830	840	850
SEQ	YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPFLSHILNSLQGLSSIHYVGKTED					
gi 217	YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPFLSHILNSLQGLSSIHYVGKTED					
	970	980	990	1000	1010	1020

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      860      870      880      890      900      910
SEQ    FISQFKRLTDAQNNYLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
      .....
gi|217 FISQFKRLTDAQNNYLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
      1030      1040      1050      1060      1070      1080

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      920      930      940      950      960      970
SEQ    VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
      .....
gi|217 VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
      1090      1100      1110      1120      1130      1140

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      980      990      1000      1010      1020      1030
SEQ    IIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGVGRTGSGKSSLGMALFRLVEPMAGRIL
      .....
gi|217 IIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGVGRTGSGKSSLGMALFRLVEPMAGRIL
      1150      1160      1170      1180      1190      1200

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      1040      1050      1060      1070      1080      1090
SEQ    IDGVDICSIGLEDLRSLKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKEI
      .....
gi|217 IDGVDICSIGLEDLRSLKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKEI
      1210      1220      1230      1240      1250      1260

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      1100      1110      1120      1130      1140      1150
SEQ    SKFPPKLLHTDVVENGGNFSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTI
      .....
gi|217 SKFPPKLLHTDVVENGGNFSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTI
      1270      1280      1290      1300      1310      1320

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      1160      1170      1180      1190      1200      1210
SEQ    REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
      .....
gi|217 REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
      1330      1340      1350      1360      1370      1380

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SEQ    LR
      ::
gi|217 LR

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1219 residues in 1 query sequences

1382 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Mon Nov 11 10:23:05 2002 done: Mon Nov 11 10:23:06 2002

Scan time: 0.050 Display time: 2.400

Function used was FASTA